Cirad rubber breeding country report (France) for the period from 2004 to 2007

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Introduction

Cirad contributes to rubber breeding in partnership with public and private organisations involved in rubber research, rubber development and rubber utilization.

Development and use of molecular genetic markers is included in this report. In vitro culture, genetic transformation, and molecular physiology mainly base on RNA analysis and expressed genes, related with the Irrdb Biotechnology group, are not included in this report.

1. Genetic resources

Concerning IRRDB 1981 germplasm, genetic and agronomical characterization carried out in cooperation with different partners, mainly Cnra (Côte d'Ivoire), was related in details in the final scientific report of STD3 project funded by European Union (French language) and summarized in the report to IRRDB meeting at Ho Chi Minh City (Vietnam) in 1997 (Clément-Demange *et al.* 1997 a,b).

Later on, information about the IRRDB 1981 germplasm was presented to IRRDB in Cirad country reports in 1999 (Haikou), 2002 (Kuala Lumpur), and 2004 (Kunming).

From diversity studies, by use of molecular genetic markers and agronomical assessment, 6 genetic groups were designed for characterizing the genetic structure of *Hevea brasiliensis* germplasm including 4 IRRDB 1981 amazonian groups, Schultes-Palmira, and Wickham populations (Seguin *et al.* 2003). From the agronomical characterization of more than 1,000 accessions in small scale trials, a working population of 287 accessions including Schultes, CNSAM, and other accessions, thereby combining genetic diversity and latex production, was designed for further works. The African conservation centre based in Côte d'Ivoire (2,847 accessions) was enriched with introductions from Malaysia and Vietnam (380 accessions from the Asian conservation centre). However, the objective of building a core collection of the available *Hevea* germplasm was not implemented yet.

The use of the Amazonian germplasm for latex production improvement, although enlarging the genetic base of *Hevea*, can be only a very long term objective due to the very low additive value and important genetic burden of those wild accessions. From the Wickham x

Amazonian crosses evaluated in small scale clonal trials (SSCT), only a very limited number of clones could be drawn for assessment in large scale clonal trials (LSCT). As far as the selection of clones for timber use is of only little interest if not combined with a reasonable latex production level, such a use of the amazonian germplasm is also for the long term.

A sample of 298 IRRDB 1981 germplasm accessions, partly belonging to the working population (121 accessions in French Guyana, and 49 accessions in Brazil), was assessed for tolerance to SALB (Le Guen *et al.* 2002). Two sets of observations were made in French Guyana, in early 1999 and late 2000, but only one set was done in Brazil in early 1999. All results exhibited a high ratio of SALB-susceptible clones among Mato Grosso origins (up to 81%), whereas a large majority (87%) of clones from Acre or Rondonia were resitant ones. The resistance of Mato Grosso clones seemed to be more unstable than that of Acre or Rondonia clones.

A Microsoft Access database named Rcc (Rubber clones Cirad) was set for storing and providing easy access to the information about accessions and rubber clones. Storing information is in process.

2. Development of molecular tools for genetic analysis

Following the development and use of RFLP co-dominant and locus-specific markers, emphasis was put on the development of microsatellite (SSR) markers that are based on targeted PCR technology. Identification of microsatellite sequences was developed at Cirad based on the building of microsatellite-enriched libraries and sequencing under a grant from Genoscope/National Sequencing Centre (Evry, France) in 1999 and 2000 (Seguin *et al.* 2001). The microsatellite sequences (472 couples of primers) belong to the public domain and are registered in the international DNA sequence database EMBL/Genbank.

Microsatellite markers have also been identified in the DNA of the fungus *Microcyclus ulei,* so allowing developing fingerprinting on *Microcyclus* strains (Le Guen *et al.* 2004).

In the framework of a Cirad project devoted to varied crops including rubber, the stability of the genetic relationships between markers and QTLs is being analysed in relationship with the different genetic groups and the genetic distance between them (« Linkage Disequilibrium » project). This will help to identify QTLs which would be available in a large range of genetic backgrounds. This research is planned for the Wickham genetic group on one hand, and for the Amazonian genetic groups on the other hand (Seguin *et al.* 2006a).

With this view, a BAC library of the clone RO38 (FX3899) has been built and is currently analysed (Piffanelli *et al.* 2003). BAC fragments, with an average size of 100 kb, are small enough to facilitate the identification of closely related markers in some tagged chromosomal regions, especially those containing genes of interest (as a comparison, a small genetic distance of 1 centi-morgan (cM) between two markers is, in average, equivalent to 700-800 kb). This will help to fine-tune the genetic mapping of genes by chromosomal walking. For instance, we recently proved the feasibility, on rubber tree, of the conversion of mapped RFLP markers into targeted PCR markers, through the identification of microsatellite markers from BAC ends sequences (Seguin *et al.* 2006a).

Applications of molecular genetic markers are clonal identification, genetic diversity analysis, parentage testing, genetic mapping for QTL approach, and linkage disequilibrium for markers-genes association studies.

3. Cirad-Michelin-Brazil (CMB) project (breeding for resistance to SALB)

The CMB project, targeted towards breeding for clones combining sustainable tolerance to SALB and economically profitable latex production, is made of 3 research components:

- Biology and epidemiology of the fungus *Microcyclus ulei*
- Genetic analysis of resistance sources in rubber
- Recombination and selection.

Field research is carried out at PEM (Plantation Edouard Michelin, an escape area with low pressure of *Microcyclus* in Mato Grosso, Brazil), PMB (Plantation Michelin de Bahia, Brazil, with a highly diversified set of aggressive strains), and French Guyana (with a limited set of strains). As added to this project, the site of PEM is also used for breeding Wickham clones for adaptation to soil and climatic suboptimal conditions (with a cold and dry season).

Starting from the germplasm formerly collected by Firestone and the IRRDB 1981 germplasm, a large set of genotypes was assessed in small scale clonal trials at Bahia for the identification of parents with resistance sources. There are currently 80 clones (from FDR, CD, CDC, MDF, MDX and IRRDB 1981 origins) selected and classified in a parental population to be used for recombination between each other and with Wickham parents. Among them, 13 clones were selected for their good general behaviour including latex production. These 13 clones, which are set in a network of large scale clonal trials, are the following:

- CD1174
- CDC56
- CDC312
- FDR4575
- FDR5240
- FDR5283
- FDR5597
- FDR5665
- FDR5788
- FDR5802
- MDX607
- MDX624
- PMB1

Table 1 provides adjusted means calculated from different trials in order to compare these clones between each other and with other clones for vigour and latex yield.

Hand pollination is carried out at PEM since 1993, and seeds are germinated at PMB for evaluating seedlings under the natural pressure of *Microcyclus* and under controlled conditions of inoculation of some poly-virulent isolates.

A first analysis of genetic resistance to SALB was carried out by QTL approach on the segregating family PB260 x RO38 (Lespinasse *et al.* 2000 a,b). RO38, alias FX3899, is issued from the female *Hevea benthamiana* parent F4542 bearing resistance to SALB. Ten different QTLs, issued from testing over five strains of the fungus, were found available in RO38, with specificity of resistance to different strains. Field evaluation against the pool of *Microcyclus* strains available in French Guyana was carried out under the real infestation conditions, and it confirmed the presence of one major QTL in genetic linkage group g13 (*M13-1bn* locus) previously found under controlled infestation (Le Guen *et al.* 2003). Complete resistance of RO38 is normally achieved when favourable alleles are present at least at the *M13-1bn* locus and also at other ancillary minor locus. Then it was shown that this major QTL was no more efficient against two widely virulent and highly aggressive strains. For one of these two strains, another QTL located on the linkage group g12 was able to reduce the aggressiveness. For the other one (isolate Pmb34), there was no more efficient resistance QTL (Seguin *et al.* 2006b, Le Guen *et al.*, 2007). Thereby, this resistance system cannot be opposed to any type of *Microcyclus* strains population and it would have to be combined complementarily with at least one other resistance source. Thus, QTL analysis on a large progeny allowed obtaining unexpected results (summarised figure 1) on genetic determinism of SALB resistance in rubber tree. This determinism appears much more complex than previously hypothesised, based on phenotypic observations.
As MDF180 was shown to exhibit a very sustainable resistance to SALB since a long time at PMB, a new investigation is currently carried out with the family PB260 x MDF180.

Going from neutral molecular markers to the study of expressed genes, a complementary candidate gene approach is now developed, based on RNA collection and analysis through Suppressive Substractive Hybridization (SSH), in order to identify genes specifically expressed in some clones susceptible or tolerant to SALB, with RNA collected at different times after controlled inoculation of *Microcyclus* isolates. EST banks are created and their sequences compared with those of genes already registered in gene banks databases. The two tolerant clones being analysed are RO38 and MDF180.

4. Genetic analysis of Wickham progenies by QTL approach in Thailand

In order to analyse the genetic bases of latex production in Wickham clones, the cross RRIM600 x PB217 was created in Thailand for genotyping the progenies and building a genetic linkage map. This is carried out in the framework of the Genmap project in cooperation with RRIT-DOA and Kasetsart University.

The two parents were chosen for their contrasted physiological behaviour, as shown by the metabolic typology of cultivated rubber clones and measured by latex diagnostic. One hypothesis is that progenies from such contrasted clones could express favourable physiological complementarities for latex production. Based on the double pseudo testcross strategy, two parental maps and a consensus map were built, with 334 progenies, 247 microsatellite markers, and 198 AFLP markers. The 18 linkage groups were assigned to the corresponding groups, equivalent to the 18 chromosomes of the *Hevea* haploid genome of the Cirad *Hevea* genetic map established with the family PB260 x RO38 and used as reference.

The total length which could be deduced from the mapping of these 445 markers was found equivalent to the 2144 cM-length initially obtained in the reference map that was built with 717 markers including 285 RFLP and 359 AFLP markers. The average length between two neighbouring markers is a little less than 5 cM, and this new map, in its current stage, appears dense enough for QTL detection (Prapan *et al.* 2006).

A clonal field trial was set in Thailand in June 2002 for assessing196 progenies of the cross. It will be studied until 2010 and targeted to the genetic analysis of the physiological parameters of the latex diagnostic which determine the metabolic typology of rubber clones. The experimental design is an "alpha-plan" (incomplete block design): it was chosen for controlling the variation of the environment, for improving the levels of the heritability of the measured agricultural traits, and for improving the estimation of the genetic values of every genotype. So far, tapping has not begun yet, and QTL detection has been initiated only for immature traits, mainly growth. As growth is a complex trait, the associated heritability appear rather low, with a maximum of 0.36 for one height measurement. First analyses for QTL detection have shown one very significant QTL associated with the trunk girth. Progenies homozygous for one recessive allele at the corresponding locus (one fourth of the population) exhibit a girth significantly lower than the other progenies (10 % lower). Thereby, this QTL could be used for screening a large number of progenies from this cross at very early stage in order to limit field evaluation to only vigorous clones. Although only preliminary, this first result is encouraging.

In Brazil, the family PR255 x PB217 was created at PEM, in the framework of the CMB project and 280 progenies were set to the field for evaluation of their physiological behaviour (latex diagnostic and metabolic typology) and their adaptation to cold climate. It is planned to develop the genetic linkage map of this family, in cooperation with the University of Campinas, in order to carry out a similar QTL approach in Brazil.

5. IRCA small scale selection in Côte d'Ivoire

The best clones of series IRCA 00 to 800 created in cooperation with CNRA and issued from hand pollination campaigns of the years 1974 to 1983 have been evaluated in two or more large scale clonal trials in Côte d'Ivoire. Only the clone IRCA871, that seemed very interesting in small scale clonal trial, has not been set in large scale trial yet.

Tables 2, 3, 4, 5, and 6 present the genetic origins of clones selected at CNRA in small scale clonal trials for series IRCA 900 (hand pollination in year 1984), 1000 (year 1985) , 1100 (year 1986) and 1200 (year 1987). Among them, the clones IRCA 908, 909, 911, 916, 919, 933, 945, 959, 966, 982, 983, 984, 986, 987, 989 , 1005, 1007, 1008, 1018, 1020, 1030, 1031 are assessed in only one large scale clonal trial per clone since 1994 and 1998 depending on the clones.

Selection among the clones of series IRCA 1300 (year 1988) and 1400 (year 1989) is to be finalized.

6. Large scale studies of rubber clones and recommendations

A short synthesis of Cirad knowledge about rubber clones studied in large scale clonal trials was presented at IRRDB meeting in Ho Chi Minh City in 2006 (Clement-Demange *et al.* 2006). Since then, updating of the data from Côte d'Ivoire was made with the collection of more accurate information about the susceptibility of clones to TPD and wind damage.

The seven clones GT1, RRIM600, PR107, PB217, PB235, PB260, and RRIC100 are used as a set of references for assessing all other clones. Among them, PB260, PB217, and RRIC100 play a key function in estates, with PB260 for the latex production of the first 10 tapping years, PB217 for the latex production of the second period of 10 tapping years, and RRIC100 for providing security in the areas affected by leaf diseases *Colletotrichum* and *Corynespora*.

In Côte d'Ivoire, the former selection of about 30 interesting clones is not to be changed but the classification of clones can be slightly modified as following :

	Class 1	Class 2	Class 3		Smallholdings
Total	**30%**	**50%**	**20%**		
Per clone	**10-20%**	**5-10%**	**2-5%**		
	PB217	**IRCA18**	**GT1**	**IRCA19**	**RRIC100**
	PB260	**IRCA41**	**PB235**	**IRCA101**	**PB217**
		IRCA109	**PR107**	**IRCA145**	**IRCA41**
		IRCA230	**RRIM600**	**IRCA427**	**IRCA230**
		IRCA317		**IRCA428**	**IRCA331**
		IRCA331	**PB324**	**IRCA523**	
		RRIC100	**PB330**	**IRCA631**	
			PC10	**IRCA733**	
			RRIM703	**IRCA804**	
			RRIM712	**IRCA840**	
			RRIM729		
			RRIM802		

The following remarks can be said :

- Clones that are not susceptible to physiological exhaustion after intensive stimulation are preferentially proposed to smallholders. IRCA41 is becoming very popular in the smallholding sector in Côte d'Ivoire.

- Clones with a tall and straight dominant trunk would be more adapted to rubber wood valorisation as Latex-Timber Clones (LTC) but such clones generally appear as the most susceptible to wind damage. Among them, PB330 exhibited impressive trunk snaps in trials. IRCA804 also appears as susceptible to wind damage. Susceptibility of PB260 is also an issue.

- Although susceptible to TPD, RRIM703 is as fast and high yielding as PB260 but also susceptible to strong benting and probably to wind damage.

- Latex yield potential of RRIM712 is not expressed during the first tapping years but later. This clone seems not much susceptible to wind damage nor TPD.

- IRCA18 which was becoming very popular in Côte d'Ivoire must be used only for a limited share due to *Corynespora* risk, especially in the East of Côte d'Ivoire.

- IRCA230 is vigorous, high yielding and with a good sucrose ratio in the latex. It was found very susceptible to *Corynespora* on a small plot in North Sumatra, and it seems susceptible to TPD after more than 10 years of tapping.

- IRCA317 is a quick starter and high yielding, but with a low sucrose ratio n the latex and it seems susceptible to TPD.

- IRCA331 confirms its high potential and low susceptibility to TPD.

- IRCA523 and IRCA733 seem susceptible to TPD.

Figure 2 shows the real distribution of the clones over a set of estates covering 70,000 ha in Africa, as inherited from the story of the last 35 years of rubber planting. Whereas GT1 has been the major clone used for security in the past, many more yielding clones are now well known and can come and replace the old ones. The IRCA breeding programme in Côte d'Ivoire has made available a new source of diversification at the level of the two leaders PB260 and PB217, and maybe a little higher for some of them.

7. Identification of clones and clonal conformity checking

Whereas vegetative multiplication through budding is a great advantage for rubber dissemination, it is also a source of inevitable mistakes along the handling of budwood, budding and planting operations.

Recognition of clones by their seeds, with assistance of a seed bank for reference, can be done only for mature seed-producing trees.

Recognition of clones by varied morphological traits has been proposed (Mercikutty *et al.* 2002; Prabhakara Rao 2005). But such methodology may be thought very dependant on the skill of some specialized technicians and rather uncertain due to the variations generated by the environment.

Cirad has developed a reference database for the checking of rubber clones by isozyme analysis, using 13 isozyme loci (Leconte *et al.* 1994, 1997). This method is efficient as far as the laboratory facilities are available on site in the plantation areas. But the fast degradation of enzymes at normal temperature, especially in the tropical rubber cropping areas, is a limitation to this technique.

For making possible the checking of clones from assumed known origin, or even for the identification of clones from unknown origin, Cirad currently develops a new reference database of patterns for 8 microsatellite markers. Due to the good stability of DNA molecule, the main advantage of this method is that gresh or slightly dried leaf samples can be sent by mail from plantation sites to any laboratory in the country or abroad for analysis. Moreover, the high polymorphism of the 8 chosen microsatellite markers provides a high discriminating

power between the genotypes that makes finding the same pattern for two different clones very improbable.

UPOV recognises only phenotypic traits for variety certification and registration, such as morphological traits, and also isozyme markers as complementary descriptors. But molecular markers such as microsatellites cannot be taken into account by UPOV so far. Whatsoever, considering the specific case of rubber, IRRDB might decide to set a service for checking the clones to the benefit of the participants to the rubber commodity channel. Microsatellites might be considered as the most accurate and powerful tool for achieving that goal.

References

Clément-Demange, A. (2006). Cirad recommendations for assisting planters in the choice of rubber clones, and suggested future activities of the IRRDB breeding group. IRRDB meeting in Ho Chi Minh City, Vietnam, 13-17 November 2006.

Clément-Demange, A., Legnaté, H., Chapuset, T., Pinard, F., and Seguin, M. (1997a). Characterization and use of the IRRDB germplasm in Ivory Coast and French Guyana: status in 1997. IRRDB 1997 Workshop in Vietnam, 14-15 October 1997.

Clément-Demange, A., Legnaté, H., Seguin, M., Boutry, M., Leconte, A., Luo, H., Chapuset, T., Pinard, F., Doumbia, A., Gobina, S., and Koffi, K. E. (1997b). STD3 germplasm *Hevea*. Contrat n° TS3-CT92-0133. Etude et caractérisation de nouvelles ressources génétiques: leur utilisation en amélioration de l'hévéa. Rapport scientifique final. Volume 1/3: Document de synthèse. Volume 2/3: Quatrième et dernière année du projet, décembre 1995-décembre 1996. Volume 3/3: Annexes. Rapport CP_SIC 769, avril 1997. Résumé (6 pages).

Clément-Demange, A., Prapan, K., Ratanawong, R., and Teerawatanasuk, K. (2006). Molecular genetic markers and rubber breeding in Thailand. 2 - Field study of the family RRIM600 x PB217 for QTL identification. Second seminar on Thai-French Rubber Cooperation. 1st - 2nd June 2006, Bangkok.

Leconte, A., Lebrun, P., Nicolas, D., and Seguin, M. (1994). Electrophoresis: application to *Hevea* clone identification. Plantations, recherche, développement 1 (2):28-36.

Leconte, A., Le Guen, V., Rodier-Goud, M., and Seguin, M. (1997). Germplasm characterization and clone identification or rubber through leaves zymogram analysis. Paper read at Seminar-Workshop on the biochemical and molecular tools for exploitation diagnostic and rubber tree improvement, at Mahidol University, October 21-24, 1997, Bangkok, Thaïland, pp. VI/1-VI/6.

Le Guen, V., Garcia, D., Mattos, C. R. R., and Clément-Demange, A. (2002). Evaluation of field resistance to *Microcyclus ulei* of a collection of Amazonian rubber tree (*Hevea brasiliensis*) germplasm. Crop Breeding and Applied Biotechnology **2**, 141-148.

Le Guen, V., Lespinasse, D., Oliver, G., Rodier Goud, M., Pinard, F., and Seguin, M. (2003). Molecular mapping of genes conferring field resistance to South American Leaf Blight (*Microcyclus ulei*) in rubber tree. Theoretical and Applied Genetics **108**, 160-167.

Le Guen, V., Rodier-Goud, M., Troispoux, V., Xiong, T., Brottier, P., Billot, C., and Seguin, M. (2004). Characterization of polymorphic microsatellite markers for *Microcyclus ulei*, causal agent of South American Leaf Blight of rubber trees. Molecular Ecology Notes **4**, 122-124.

Le Guen, V., Garcia, D., Mattos, C.R.R., Doaré, F., Lespinasse, D., Seguin, M. (2007) Bypassing of a polygenic *Microcyclus ulei* resistance in rubber tree, analyzed by QTL detection, New Phytologist 173: 335-345.

Lespinasse, D., Grivet, L., Troispoux, V., Rodier Goud, M., Pinard, F., and Seguin, M. (2000a). Identification of QTLs involved in the resistance to South American Leaf Blight (*Microcyclus ulei*) in the rubber tree. Theoretical and applied genetics **100**, 975-984.

Lespinasse, D., Rodier, G. M., Grivet, L., Leconte, A., Legnate, H., and Seguin, M. a. (2000b). A saturated genetic linkage map of rubber tree (*Hevea* spp.) based on RFLP, AFLP, microsatellite, and isozyme markers. Theoretical and Applied Genetics **100**, 127-138.

Mercykutty, V. C., Marattukalam, J. G., Saraswathyamma, C. K., and Meenakumari, T. (2002). Identification of *Hevea* clones. A manual. Rubber Research Institute of India, Botany Division, ISBN 81-87439-03-3, 103 pp.

Piffanelli, P., Noa-Carrazana, J.-C., *et al.* (2003) BACTROP: a platform of genomic resources to study organization and evolution of tropical crop species. In: 7th International Congress of Plant Molecular Biology, June 23-28, Barcelona, Spain, 2003, ISPMB, pp. 58

Prabhakara Rao, G., Abraham, S. T., Reghu, C. P., and Varghese, Y. A. (2005). Descriptors for rubber (*Hevea brasiliensis* Willd. ex Adr. de Juss.) Muell. Arg. Rubber Research Institute of India, Kottayam, Kerala, India. ISBN 81-87439-10-6.

Prapan, K., Lekawipat, N., Weber, C., Rodier-Goud, M., Clément-Demange, A., and Seguin, M. (2006). Molecular genetic markers and rubber breeding in Thailand: 1 - Genetic mapping of the family RRIM600 x PB217 by use of microsatellite markers. Second seminar on Thai-French Rubber Cooperation, 1st - 2nd June 2006, Bangkok.

Seguin, M., Flori, A., Legnate, H. and Clément-Demange, A. (2003). Rubber tree (*Hevea brasiliensis*). In : « Hamon, P., Seguin, M., Perrier, X., and Glaszmann, J.-C. Eds. "Genetic diversity of cultivated tropical plants », Repères, Cirad, pp. 277-305.

Seguin, M., Attard, A. *et al.* (2006a). Analysis of linkage disequilibrium patterns in perennial or annual, autogamous or allogamous plant species. Paper read at 6ème Colloque National du BRG. Ressources Génétiques : des Ressources Partagées, at La Rochelle, 2-4 October 2006. (English abstract)

Seguin, M., Rodier-Goud, M., Doaré, F., Lespinasse, D. and Le Guen V. Genetic mapping and QTL analysis of Microcyclus ulei resistance in rubber tree (Hevea spp.), in P-GEM5, Venice, October 11-14 2006, 2006, pp. poster n°6-25

Tables and figures

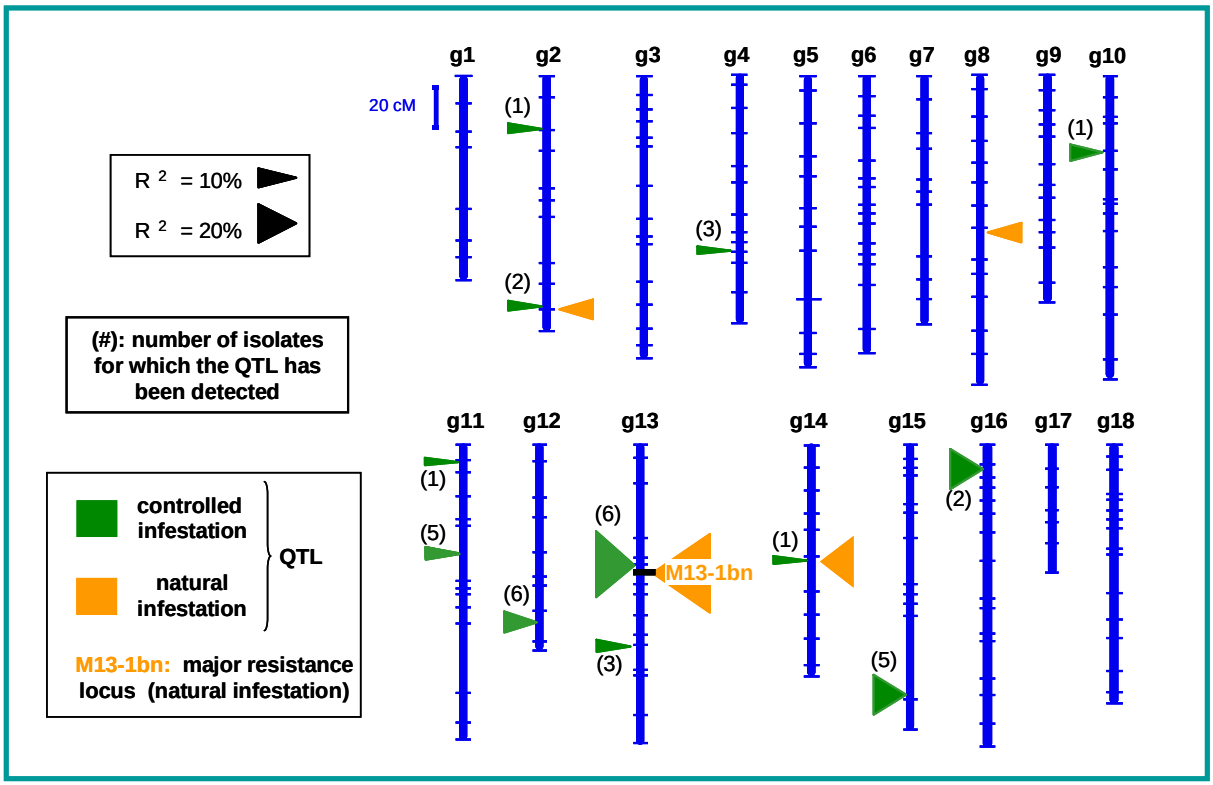


Fig. 1: Location on the RO38 parental map of the QTLs detected in controlled (8 *M. ulei* isolates) or natural conditions of infestation. g#: linkage group / chromosome numbers according to the *Hevea* reference map (from Seguin et al. 2006b).

Table 1: Adjusted means of clones assessed in CMB project, including the 13 clones developed in large scale clonal trials.

Clone	Circ.	Prod		Clone	Circ.	Prod		Clone	Circ.	Prod
Mini	19.17	174.3		MDX45	30.08	666.9		FDR5162	28.61	410.3
Maxi	42.30	1351.0		FDR4773	28.71	664.5		MDX239	32.15	410.1
FDR1057	21.10	**1351.0**		FDR3094	33.40	662.3		MDX83	29.57	409.9
FDR4575	33.68	1200.3		SIAL839	21.47	654.8		CDC32	34.82	396.3
FDR4127	24.51	1110.6		**MDX607**	36.47	653.8		FX2784	30.99	394.7
FDR5597	32.74	1087.7		FDR4229	32.22	640.5		MDX50	30.34	393.7
MDX624	**42.30**	1087.3		**CDC56**	33.59	633.1		TP21	33.87	391.6
FDR5240	34.37	1081.5		TP808	31.41	613.3		CDC871	35.99	388.8
FDR2010	32.00	1050.8		TP1003	33.51	609.4		IRCA573	21.99	386.2
FDR6099	33.49	1019.9		**FDR5283**	36.43	609.4		TP1004	32.46	379.3
CD38	29.08	1015.2		TP7819	34.13	596.4		FDX496	30.35	376.2
FDR6003	26.27	1007.3		GU158	23.92	593.6		FDR5145	31.22	373.8
FDR5953	30.91	980.8		CDC347	34.68	592.1		TP39	38.60	373.1
FDR4151	31.00	936.1		MDX98	31.24	586.4		FX3028	25.99	367.4
CDC832	26.39	925.6		FDR1066	20.14	577.4		FDR5763	33.40	367.1
MDX608	33.71	918.7		**FDR5665**	38.39	575.4		CDC555	33.23	358.0
MDX42	27.54	873.3		IT531	35.68	573.3		CDC318	37.87	354.0
RO38	31.93	869.3		CD1101	31.29	572.9		TP65	27.49	351.1
FDR650	27.99	857.1		FDR6031	26.62	567.8		F4512	31.11	350.6
FDR5894	30.25	837.4		CDC219	33.18	565.8		TP166	38.67	350.2
CDC943	34.26	836.0		GU235	28.21	557.3		MDX17	29.40	342.3
CDC919	31.48	819.0		FDR3269	32.99	554.0		FX2261	21.74	341.7
MDX15	22.15	799.5		FDR4461	33.18	548.7		MDX25	30.18	340.7
FDR6095	33.42	798.0		FDR5217	28.69	547.2		FX25	31.24	332.0
CDC12	23.69	793.9		FDR5680	29.93	536.9		CDC689	30.71	320.3
FDR233	32.82	789.6		FX4098	26.78	535.7		MDX49	24.93	316.3
CDC273	27.10	788.0		IT537	33.39	511.9		RRIM725	19.26	304.5
FDR6098	36.67	786.1		TP7818	30.82	509.4		FX3864	**19.17**	293.1
FDR5792	28.07	771.4		CD1161	36.35	507.3		MDX495	36.63	289.5
FDR5794	32.76	767.2		MDX31	29.26	506.6		FDR5175	28.67	282.4
CD1130	33.98	760.0		GU507	34.22	505.6		SIAL893	26.06	273.2
FDR5429	29.35	757.7		FDR5856	37.26	502.8		IRCA621	22.51	270.6
FDR5211	27.35	752.2		FDR4459	31.50	500.8		MDF180	32.87	265.6
CDC846	33.51	751.2		CDC1534	29.35	483.8		CDC557	27.54	253.1
CDC308	36.31	744.6		CDC986	27.78	482.8		MDX24	21.89	246.8
FDR3275	28.67	742.6		FDR3642	27.51	475.4		FX4049	33.64	245.5
FDR5189	27.80	734.6		MDX87	30.40	475.2		CDC547	35.29	209.6
CDC358	29.21	734.2		IAN6158	21.56	470.1		CDC965	36.01	200.0
CDC429	32.59	728.8		**FDR5802**	37.85	465.4		FDR3376	33.88	**174.3**
TP875	32.40	721.5		CD1169	38.98	464.1				
FDR5643	32.49	692.9		IRCA519	22.89	422.2				
FDR5788	37.87	679.6		**CD1174**	33.68	417.8				
TP749	33.17	679.0		MDX96	31.50	415.9				
CDC312	36.63	676.1		FDR5465	30.83	411.6				

Table 2: Genetic origins of the early selection of series IRCA900.

Clone	Genetic origin
IRCA908	PB235 x RRIC103
IRCA909	PB235 x RRIM703
IRCA911	GT1 x RRIM703
IRCA916	PB235 x PFB5
IRCA919	PB5/51 x RO61
IRCA933	PB235 x RRIM703
IRCA945	GT1 x RRIM703
IRCA959	PB5/51 x RO38
IRCA966	PB235 x PFB5
IRCA982	PB5/51 x RRIC100
IRCA983	PB5/51 x RRIC103
IRCA984	PB5/51 x RRIC103
IRCA986	GT1 x PB260
IRCA987	PB5/51 x RRIC100
IRCA989	GT1 x PB260

Table 3: Genetic origins of the complementary selection of series IRCA900.

Clones	Genetic origins
IRCA930	PB235 x RRIM703
IRCA931	PB235 x RRIM703
IRCA932	PB235 x RRIM703
IRCA933	PB235 x RRIM703
IRCA936	PB235 x RRIC103
IRCA937	PB235 x RRIC103
IRCA938	GT1 x RRIM703
IRCA944	GT1 x RRIM703
IRCA950	GT1 x RRIM703
IRCA951	GT1 x RRIM703
IRCA952	GT1 x PB260
IRCA957	PB5/51 x RO61
IRCA961	PB235 x PFB5
IRCA962	PB235 x PFB5
IRCA963	PB235 x PFB5
IRCA965	PB235 x PFB5
IRCA968	PB235 x PFB5
IRCA973	PB235 x PFB5
IRCA974	PB235 x PFB5
IRCA975	PB235 x PFB5

Table 4: Genetic origins of the selection of series IRCA1000.

Clones	Genetic origins
IRCA1003	PB5/51 x PR107
IRCA1005	PB260 x GU198
IRCA1007	PB260 x RRIM703
IRCA1008	PB260 x RRIM703
IRCA1009	PB260 x RRIM703
IRCA1010	PB260 x RRIM703
IRCA1017	PB235 x RRIC130
IRCA1018	PB235 x RRIC130
IRCA1020	PB235 x RRIC102
IRCA1021	PB235 x RRIC102
IRCA1022	PB235 x MDX17
IRCA1023	PB235 x AVROS2037
IRCA1027	PB235 x P122
IRCA1029	PB217 x RRIM703
IRCA1031	PB217 x RRIM703
IRCA1033	PB217 x RRIM703
IRCA1035	PB217 x RRIM703
IRCA1043	GT1 x PB217
IRCA1045	GT1 x RRIM701
IRCA1046	GT1 x PB217
IRCA1052	AVROS2037 x RRIM703

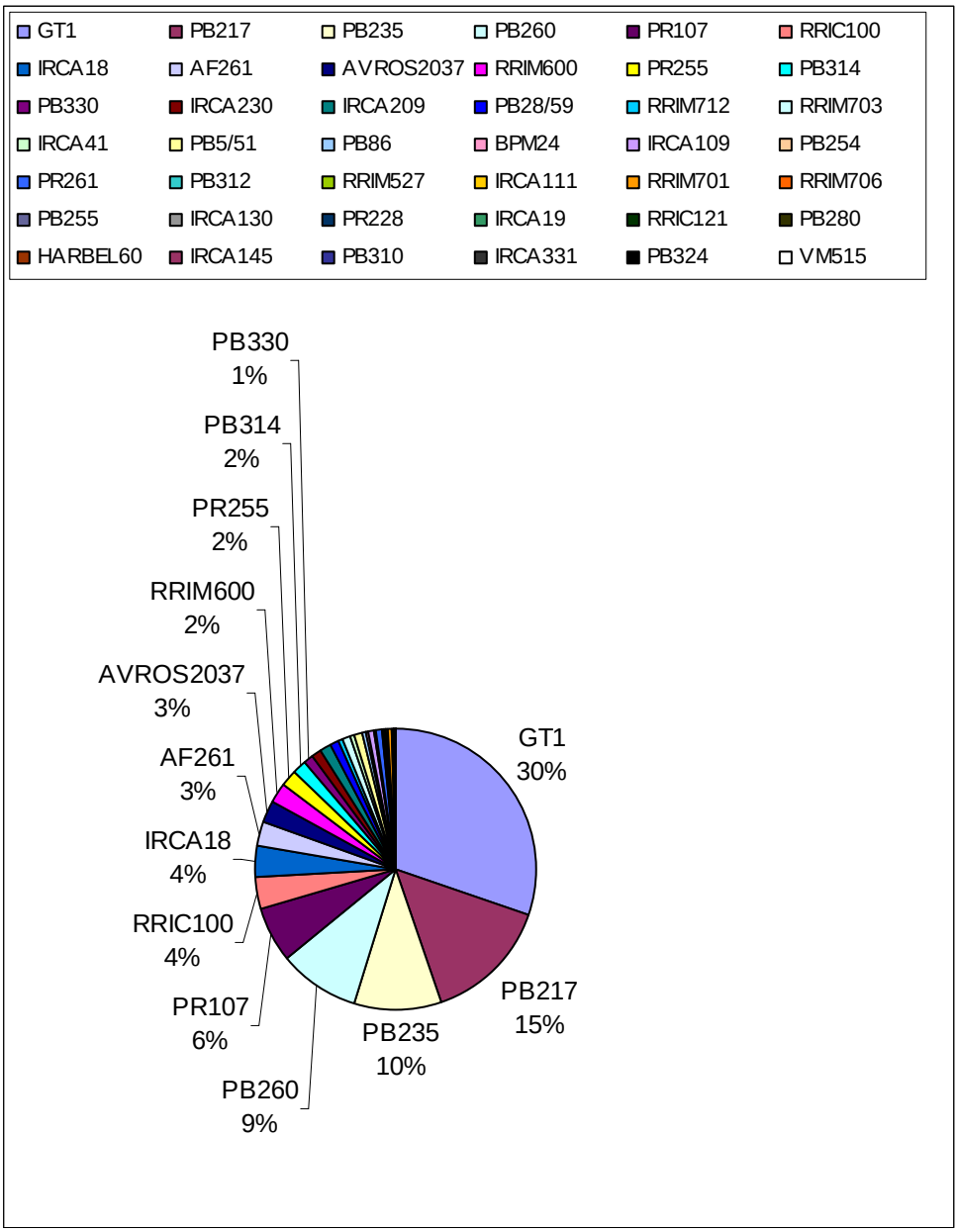
Table 5: Genetic origins of the early selection of series IRCA1100.

Clones	Genetic origins
IRCA1100	RRIC110 x RRIM703
IRCA1102	RRIC102 x PB217
IRCA1131	PB235 x RRIC101
IRCA1138	RRIC110 x IRCA111
IRCA1152	PB5/51 x GU969
IRCA1153	PB260 x RRIC101
IRCA1157	PB260 x RRIC110
IRCA1160	PB5/51 x GU86
IRCA1163	PB260 x RRIC102

Table 6: Genetic origins of the selection of series IRCA1200.

Clones	Origines génétiques
IRCA1202	PB260 x RO/CM/12/2
IRCA1203	PB235 x RRIM703
IRCA1210	PB5/51 x PR107
IRCA1220	RRIM703 x PB260
IRCA1226	PB260 x RO/I/110
IRCA1227	PB260 x RO/I/110
IRCA1235	PB5/51 x IR22
IRCA1236	PB5/51 x IR22
IRCA1244	PB260 x IRCA209
IRCA1245	PB235 x RRIM600
IRCA1247	PB235 x RRIM703
IRCA1248	PB5/51 x IR22
IRCA1249	PB5/51 x IR22
IRCA1250	PB5/51 x IR22
IRCA1254	PB5/51 x IR22
IRCA1255	PB5/51 x PR228
IRCA1259	PB5/51 x IR22
IRCA1260	PB5/51 x IR22
IRCA1262	PB5/51 x IR22
IRCA1274	PB5/51 x PR228

Figure 2: Clonal distribution over a set of surveyed estates in Africa, for a total of 70,000 ha.



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